

Listing of Claims:

Claims 1-46 (canceled) without prejudice

Claim 47. (New) An isolated polynucleotide sequence comprising:

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- (a) a nucleotide sequence of SEQ ID NO: 1;
 - (b) a nucleotide sequence of SEQ ID NO: 4;
 - (c) a nucleotide sequence encoding a UDP-glucose binding domain;
 - (d) a sequence conservative variant of (a), (b), or (c); or
 - (e) a truncated nucleotide sequence of (a), (b), or (c) encoding a functional domain of cellulose synthase.

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Claim 49. (New) A vector comprising a polynucleotide as set forth in claim 47.

Claim 50. (New) A transgenic plant comprising a polynucleotide as set forth in claim 47.

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Claim 67. (New) A isolated polynucleotide encoding a polypeptide comprising:

- (a) an amino acid sequence of SEQ ID NO:2;
- (b) an amino acid sequence of SEQ ID NO:5;
- (c) an amino acid sequence comprising 75% similarity to (a) or (b);
- (d) an amino acid sequence comprising a UDP-glucose binding domain exhibiting cellulose synthase functional activity independent of other portions of the cellulose synthase polypeptide; or
- (e) a function-conservative variant of (a), (b), or (d).

41
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Claim 68. (New) A method of altering a characteristic of a plant comprising incorporating into the genome of the plant a nucleotide sequence encoding cellulose synthase, such that when the nucleotide sequence is expressed in the plant, the characteristic of the plant is altered, wherein the characteristic includes at least one of altered growth, altered cellulose content, altered lignin content, and altered strength of juvenile wood and fiber, and combinations thereof compared to a control plant that is not transformed with the nucleotide sequence.

Claim 69. (New) The method as set forth in claim 68 wherein the nucleotide sequence is in the anti-sense orientation.

Claim 70. (New) The method as set forth in claim 68 wherein the nucleotide sequence is in the sense orientation.

Claim 71. (New) The method as set forth in claim 68 wherein the nucleotide sequence is heterologous.

Claim 72. (New) The method as set forth in claim 68 wherein the nucleotide sequence is homologous.

Claim 73. (New) The method as set forth in claim 68 wherein the nucleotide sequence comprises:

- (a) a nucleotide sequence of SEQ ID NO: 1;
- (b) a nucleotide sequence of SEQ ID NO: 4;
- (c) a nucleotide sequence encoding a UDP-glucose binding domain;
- (d) a sequence conservative variant of (a), (b), or (c); or
- (e) a truncated nucleotide sequence of (a), (b), or (c) encoding a functional domain of cellulose synthase.

43
Claim 74. (New) The method as set forth in claim 68 wherein the plant is a tree.

cont. Claim 75. (New) The method as set forth in claim 74 wherein the tree is an angiosperm.

Claim 76. (New) The method as set forth in claim 74 wherein the tree is a gymnosperm.

Claim 77. (New) The method as set forth in claim 68 wherein the altered growth is accelerated growth.

Claim 78. (New) The method as set forth in claim 68 wherein the altered cellulose content is increased cellulose content or an increased ratio of cellulose to lignin in a cell.

Claim 79. (New) The method as set forth in claim 78 wherein the cellulose is characterized by an increase in crystalline content.

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Claim 80. (New) The method as set forth in claim 68 wherein the altered lignin content is decreased lignin content or a decreased ratio of lignin to cellulose in a cell.

Claim 81. (New) The method as set forth in claim 68 wherein the altered strength is improved mechanical strength.

Claim 82. (New) The method as set forth in claim 68 wherein the nucleotide sequence encodes a polypeptide comprising:

- (a) the amino acid sequence of SEQ ID NO:2;
- (b) the amino acid sequence of SEQ ID NO:5;
- (c) an amino acid sequence comprising 75% similarity to (a) or (b);

- (d) an amino acid sequence comprising a UDP-glucose binding domain exhibiting cellulose synthase functional activity independent of other portions of the cellulose synthase polypeptide; or
- (e) a function conservative variant of (a), (b), or (d).

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Claim 83. (New) The method as set forth in claim 68 wherein the nucleotide sequence is operatively linked to a promoter.

Claim 84. (New) The method as set forth in claim 83 wherein the promoter is a plant promoter, or a transcription factor binding domain thereof.

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Claim 85. (New) The method as set forth in claim 83 wherein the promoter is selected from constitutive promoters, tissue-specific promoters and developmental-specific plant promoters.

Claim 86. (New) The method as set forth in claim 83 wherein the promoter is Cauliflower Mosaic Virus 35S, 4CL, cellulose synthase promoter, *PtCelAP* or terminal flower promoter.

Claim 87. (New) A plant produced by the method as set forth in claim 68.

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Claim 126. (New) A method of altering a characteristic of a plant comprising the step of incorporating into the genome of the plant a nucleotide sequence encoding a UDP-glucose

catalytic subunit, such that when the nucleotide sequence is expressed in the plant, the characteristic of the plant is altered, wherein the characteristic includes at least one of accelerated plant growth, increased cellulose content, decreased lignin content, and improved strength of juvenile wood and fiber, and combinations thereof compared to a control plant that is not transformed with the nucleotide sequence.

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Claim 127. (New) The method as set forth in claim 126 wherein the catalytic s subunit comprises a conserved sequence, wherein the sequence is QVLRW.

Claim 128. (New) The method as set forth in claim 126 wherein the altered characteristic is accelerated growth.

Claim 129. (New) The method as set forth in claim 126 wherein the altered characteristic is increased cellulose content.

Claim 130. (New) The method as set forth in claim 126 wherein the altered characteristic is decreased lignin content.

Claim 131. (New) The method as set forth in claim 126 wherein the altered characteristic is improved strength of juvenile wood and fiber.

Claim 132. (New) A plant produced by the method as set forth in claim 126.

Claim 133. (New) A method as set forth in claim 126 wherein the plant is a tree.

Claim 134. (New) A tree produced by the method as set forth in claim 133.

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Claim 149. (New) A plant having a characteristic genetically altered through incorporation into the genome of the plant a nucleotide sequence encoding cellulose synthase, such that when the nucleotide sequence is expressed in the plant, the characteristic of the plant is altered, wherein the characteristic includes at least one of altered growth,

altered lignin content, altered cellulose content, and altered strength of juvenile wood and fiber, and combinations thereof compared to a control plant that is not transformed with the nucleotide sequence.

Claim 150. (New) The plant as set forth in claim 149 wherein the nucleotide sequence is in the anti-sense orientation.

Claim 151. (New) The plant as set forth in claim 149 wherein the nucleotide sequence is in the sense orientation.

Claim 152. (New) The plant as set forth in claim 149 wherein the nucleotide sequence is heterologous.

Claim 153. (New) The plant as set forth in claim 149 wherein the nucleotide sequence is homologous.

Claim 154. (New) The plant as set forth in claim 149 wherein the nucleotide sequence comprises:

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- (a) a nucleotide sequence of SEQ ID NO: 1;
 - (b) a nucleotide sequence of SEQ ID NO: 4;
 - (c) a nucleotide sequence encoding a UDP-glucose binding domain;
 - (d) a sequence conservative variant of (a), (b), or (c); or
 - (e) a truncated nucleotide sequence of (a), (b), or (c) encoding a functional domain of cellulose synthase.

Claim 155. (New) The plant as set forth in claim 149 wherein the plant is a tree.

Claim 156. (New) The plant as set forth in claim 155 wherein the tree is an angiosperm.

Claim 157. (New) The plant as set forth in claim 155 wherein the tree is a gymnosperm.

Claim 158. (New) The plant as set forth in claim 149 wherein the altered growth is accelerated growth.

Claim 159. (New) The plant as set forth in claim 149 wherein the altered cellulose content is increased cellulose content or an increased ratio of cellulose to lignin in cells.

Claim 160. (New) The plant as set forth in claim 159 wherein the cellulose is characterized by an increase in crystalline content.

Claim 161. (New) The plant as set forth in claim 149 wherein the altered lignin content is decreased lignin content or a decreased ratio of lignin to cellulose in the cells.

Claim 162. (New) The plant as set forth in claim 149 wherein the nucleotide sequence encodes a polypeptide comprising:

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- (a) the amino acid sequence of SEQ ID NO:2;
 - (b) the amino acid sequence of SEQ ID NO:5,
 - (c) an amino acid sequence comprising 75% similarity to (a) or (b);
 - (d) an amino acid sequence comprising a UDP-glucose binding domain exhibiting Cellulose synthase functional activity independent of other portions of the Cellulose synthase polypeptide; or
 - (e) a function-conservative variant of (a), (b), or (d).

Claim 163. (New) The plant as set forth in claim 149 wherein the nucleotide sequence is operatively linked to a promoter.

Claim 164. (New) The plant as set forth in claim 163 wherein the promoter is a plant promoter, or a transcription factor binding domain thereof.

Claim 165. (New) The plant as set forth in claim 163 wherein the promoter is selected from constitutive promoters, tissue-specific promoters and developmental-specific plant promoters.

Claim 166. (New) The plant as set forth in claim 163 wherein the promoter is Cauliflower Mosaic Virus 35S, 4CL, cellulose synthase promoter, *PtCelAP* or terminal flower promoter.